

SEQUENCE LISTING

<110> Cihlar, Tomas

<120> NOVEL GENE ENCODING ORGANIC ANION TRANSPORTER

<130> 240.1PC

<140> unassigned

<141> 1999-06-10

<150> 60/088,864

<151> 1998-06-11

<150> 60/132,267

<151> 1999-05-03

<160> 10

<170> PatentIn Ver. 2.0

<210> 1

<211> 2123

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: This information
is not available.

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<221> CDS

<222> (263)..(1912)

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ggactcagct cccgggaagc aaccagctg cggaggcaac ggcagtgtg ctctccagc 180

gaaggacagc aggcaggcag acagacagag gtctggggac tggaaggcct cagccccag 240

ccactgggct gggcctggcc ca atg gcc ttt aat gac ctc ctg cag cag gtg 292

Met Ala Phe Asn Asp Leu Leu Gln Gln Val
1 5 10

ggg ggt gtc ggc cgc ttc cag cag atc cag gtc acc ctg gtg gtc ctc 340

Gly Gly Val Gly Arg Phe Gln Gln Ile Gln Val Thr Leu Val Val Leu
15 20 25

ccc	ctg	ctc	ctg	atg	gct	tct	cac	aac	acc	ctg	cag	aac	ttc	act	gct	388
Pro	Leu	Leu	Leu	Met	Ala	Ser	His	Asn	Thr	Leu	Gln	Asn	Phe	Thr	Ala	
			30					35					40			
gcc	atc	cct	acc	cac	cac	tgc	cgc	ccg	cct	gcc	gat	gcc	aac	ctc	agc	436
Ala	Ile	Pro	Thr	His	His	Cys	Arg	Pro	Pro	Ala	Asp	Ala	Asn	Leu	Ser	
		45					50					55				
aag	aac	ggg	ggg	ctg	gag	gtc	tgg	ctg	ccc	cgg	gac	agg	cag	ggg	cag	484
Lys	Asn	Gly	Gly	Leu	Glu	Val	Trp	Leu	Pro	Arg	Asp	Arg	Gln	Gly	Gln	
	60					65					70					
cct	gag	tcc	tgc	ctc	cgc	ttc	acc	tcc	ccg	cag	tgg	gga	ctg	ccc	ttt	532
Pro	Glu	Ser	Cys	Leu	Arg	Phe	Thr	Ser	Pro	Gln	Trp	Gly	Leu	Pro	Phe	
	75				80					85					90	
ctc	aat	ggc	aca	gaa	gcc	aat	ggc	aca	ggg	gcc	aca	gag	ccc	tgc	acc	580
Leu	Asn	Gly	Thr	Glu	Ala	Asn	Gly	Thr	Gly	Ala	Thr	Glu	Pro	Cys	Thr	
			95						100					105		
gat	ggc	tgg	atc	tat	gac	aac	agc	acc	ttc	cca	tct	acc	atc	gtg	act	628
Asp	Gly	Trp	Ile	Tyr	Asp	Asn	Ser	Thr	Phe	Pro	Ser	Thr	Ile	Val	Thr	
			110					115					120			
gag	tgg	gac	ctt	gtg	tgc	tct	cac	agg	gcc	cta	cgc	cag	ctg	gcc	cag	676
Glu	Trp	Asp	Leu	Val	Cys	Ser	His	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln	
		125					130					135				
tcc	ttg	tac	atg	gtg	ggg	gtg	ctg	ctc	gga	gcc	atg	gtg	ttc	ggc	tac	724
Ser	Leu	Tyr	Met	Val	Gly	Val	Leu	Leu	Gly	Ala	Met	Val	Phe	Gly	Tyr	
	140					145					150					
ctt	gca	gac	agg	cta	ggc	cgc	cgg	aag	gta	ctc	atc	ttg	aac	tac	ctg	772
Leu	Ala	Asp	Arg	Leu	Gly	Arg	Arg	Lys	Val	Leu	Ile	Leu	Asn	Tyr	Leu	
	155				160					165					170	
cag	aca	gct	gtg	tca	ggg	acc	tgc	gca	gcc	ttc	gca	ccc	aac	ttc	ccc	820
Gln	Thr	Ala	Val	Ser	Gly	Thr	Cys	Ala	Ala	Phe	Ala	Pro	Asn	Phe	Pro	
			175						180					185		
atc	tac	tgc	gcc	ttc	cgg	ctc	ctc	tgc	ggc	atg	gct	ctg	gct	ggc	atc	868
Ile	Tyr	Cys	Ala	Phe	Arg	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Gly	Ile	
		190						195				200				
tcc	ctc	aac	tgc	atg	aca	ctg	aat	gtg	gag	tgg	atg	ccc	att	cac	aca	916
Ser	Leu	Asn	Cys	Met	Thr	Leu	Asn	Val	Glu	Trp	Met	Pro	Ile	His	Thr	
		205					210					215				
cgg	gcc	tgc	gtg	ggc	acc	ttg	att	ggc	tat	gtc	tac	agc	ctg	ggc	cag	964
Arg	Ala	Cys	Val	Gly	Thr	Leu	Ile	Gly	Tyr	Val	Tyr	Ser	Leu	Gly	Gln	
	220					225					230					

ttc ctc ctg gct ggt gtg gcc tac gct gtg ccc cac tgg cgc cac ctg	1012
Phe Leu Leu Ala Gly Val Ala Tyr Ala Val Pro His Trp Arg His Leu	
235 240 245 250	
cag cta ctg gtc tct gcg cct ttt ttt gcc ttc ttc atc tac tcc tgg	1060
Gln Leu Leu Val Ser Ala Pro Phe Phe Ala Phe Phe Ile Tyr Ser Trp	
255 260 265	
ttc ttc att gag tgc gcc cgc tgg cac tcc tcc tcc ggg agg ctg gac	1108
Phe Phe Ile Glu Ser Ala Arg Trp His Ser Ser Ser Gly Arg Leu Asp	
270 275 280	
ctc acc ctg agg gcc ctg cag aga gtc gcc cgg atc aat ggg aag cgg	1156
Leu Thr Leu Arg Ala Leu Gln Arg Val Ala Arg Ile Asn Gly Lys Arg	
285 290 295	
gaa gaa gga gcc aaa ttg agt atg gag gta ctc cgg gcc agt ctg cag	1204
Glu Glu Gly Ala Lys Leu Ser Met Glu Val Leu Arg Ala Ser Leu Gln	
300 305 310	
aag gag ctg acc atg ggc aaa ggc cag gca tgc gcc atg gag ctg ctg	1252
Lys Glu Leu Thr Met Gly Lys Gly Gln Ala Ser Ala Met Glu Leu Leu	
315 320 325 330	
cgc tgc ccc acc ctc cgc cac ctc ttc ctc tgc ctc tcc atg ctg tgg	1300
Arg Cys Pro Thr Leu Arg His Leu Phe Leu Cys Leu Ser Met Leu Trp	
335 340 345	
ttt gcc act agc ttt gca tac tat ggg ctg gtc atg gac ctg cag ggc	1348
Phe Ala Thr Ser Phe Ala Tyr Tyr Gly Leu Val Met Asp Leu Gln Gly	
350 355 360	
ttt gga gtc agc atc tac cta atc cag gtg atc ttt ggt gct gtg gac	1396
Phe Gly Val Ser Ile Tyr Leu Ile Gln Val Ile Phe Gly Ala Val Asp	
365 370 375	
ctg cct gcc aag ctt gtg ggc ttc ctt gtc atc aac tcc ctg ggt cgc	1444
Leu Pro Ala Lys Leu Val Gly Phe Leu Val Ile Asn Ser Leu Gly Arg	
380 385 390	
cgg cct gcc cag atg gct gca ctg ctg ctg gca ggc atc tgc atc ctg	1492
Arg Pro Ala Gln Met Ala Ala Leu Leu Leu Ala Gly Ile Cys Ile Leu	
395 400 405 410	
ctc aat ggg gtg ata ccc cag gac cag tcc att gtc cga acc tct ctt	1540
Leu Asn Gly Val Ile Pro Gln Asp Gln Ser Ile Val Arg Thr Ser Leu	
415 420 425	
gct gtg ctg ggg aag ggt tgt ctg gct gcc tcc ttc aac tgc atc ttc	1588
Ala Val Leu Gly Lys Gly Cys Leu Ala Ala Ser Phe Asn Cys Ile Phe	
430 435 440	

ctg tat act ggg gaa ctg tat ccc aca atg atc cgg cag aca ggc atg 1636
Leu Tyr Thr Gly Glu Leu Tyr Pro Thr Met Ile Arg Gln Thr Gly Met
445 450 455

gga atg ggc agc acc atg gcc cga gtg ggc agc atc gtg agc cca ctg 1684
Gly Met Gly Ser Thr Met Ala Arg Val Gly Ser Ile Val Ser Pro Leu
460 465 470

gtg agc atg act gcc gag ctc tac ccc tcc atg cct ctc ttc atc tac 1732
Val Ser Met Thr Ala Glu Leu Tyr Pro Ser Met Pro Leu Phe Ile Tyr
475 480 485 490

ggt gct gtt cct gtg gcc gcc agc gct gtc act gtc ctc ctg cca gag 1780
Gly Ala Val Pro Val Ala Ala Ser Ala Val Thr Val Leu Leu Pro Glu
495 500 505

acc ctg ggc cag cca ctg cca gac acg gtg cag gac ctg gag agc agg 1828
Thr Leu Gly Gln Pro Leu Pro Asp Thr Val Gln Asp Leu Glu Ser Arg
510 515 520

aaa ggg aaa cag acg cga cag caa caa gag cac cag aag tat atg gtc 1876
Lys Gly Lys Gln Thr Arg Gln Gln Gln Glu His Gln Lys Tyr Met Val
525 530 535

cca ctg cag gcc tca gca caa gag aag aat gga ctc tgaggactga 1922
Pro Leu Gln Ala Ser Ala Gln Glu Lys Asn Gly Leu
540 545 550

gaagggggcct tacagaaccc taaagggagg gaaggtccta caggtctccg gccacccaca 1982

caaggaggag gaagaggaaa tggtgaccca agtgtggggg ttgtggttca ggaaagcatc 2042

ttcccagggg tccacctccc ttataaaacc ccaccagaac cacatcatta aaagggtttga 2102

ctgcgaaaaa aaaaaaaaaa a 2123

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<211> 550
<212> PRT
<213> Unknown

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20 25 30

Ser His Asn Thr Leu Gln Asn Phe Thr Ala Ala Ile Pro Thr His His
35 40 45

Cys	Arg	Pro	Pro	Ala	Asp	Ala	Asn	Leu	Ser	Lys	Asn	Gly	Gly	Leu	Glu	50	55	60
Val	Trp	Leu	Pro	Arg	Asp	Arg	Gln	Gly	Gln	Pro	Glu	Ser	Cys	Leu	Arg	65	70	75
Phe	Thr	Ser	Pro	Gln	Trp	Gly	Leu	Pro	Phe	Leu	Asn	Gly	Thr	Glu	Ala	85	90	95
Asn	Gly	Thr	Gly	Ala	Thr	Glu	Pro	Cys	Thr	Asp	Gly	Trp	Ile	Tyr	Asp	100	105	110
Asn	Ser	Thr	Phe	Pro	Ser	Thr	Ile	Val	Thr	Glu	Trp	Asp	Leu	Val	Cys	115	120	125
Ser	His	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln	Ser	Leu	Tyr	Met	Val	Gly	130	135	140
Val	Leu	Leu	Gly	Ala	Met	Val	Phe	Gly	Tyr	Leu	Ala	Asp	Arg	Leu	Gly	145	150	155
Arg	Arg	Lys	Val	Leu	Ile	Leu	Asn	Tyr	Leu	Gln	Thr	Ala	Val	Ser	Gly	165	170	175
Thr	Cys	Ala	Ala	Phe	Ala	Pro	Asn	Phe	Pro	Ile	Tyr	Cys	Ala	Phe	Arg	180	185	190
Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Gly	Ile	Ser	Leu	Asn	Cys	Met	Thr	195	200	205
Leu	Asn	Val	Glu	Trp	Met	Pro	Ile	His	Thr	Arg	Ala	Cys	Val	Gly	Thr	210	215	220
Leu	Ile	Gly	Tyr	Val	Tyr	Ser	Leu	Gly	Gln	Phe	Leu	Leu	Ala	Gly	Val	225	230	235
Ala	Tyr	Ala	Val	Pro	His	Trp	Arg	His	Leu	Gln	Leu	Leu	Val	Ser	Ala	245	250	255
Pro	Phe	Phe	Ala	Phe	Phe	Ile	Tyr	Ser	Trp	Phe	Phe	Ile	Glu	Ser	Ala	260	265	270
Arg	Trp	His	Ser	Ser	Ser	Gly	Arg	Leu	Asp	Leu	Thr	Leu	Arg	Ala	Leu	275	280	285
Gln	Arg	Val	Ala	Arg	Ile	Asn	Gly	Lys	Arg	Glu	Glu	Gly	Ala	Lys	Leu	290	295	300
Ser	Met	Glu	Val	Leu	Arg	Ala	Ser	Leu	Gln	Lys	Glu	Leu	Thr	Met	Gly	305	310	315

[illegible] $\langle 220 \rangle$

<223> Description of Unknown Organism: This information
is not available.

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tgacctctcg cagcagg 77

<210> 4
<211> 51
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: This information
is not available.

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<210> 5
<211> 9
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown Organism: This information
is not available.

<400> 5
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<210> 6
<211> 25
<212> DNA
<213> Unknown

<220>
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<210> 7
<211> 26
<212> DNA
<213> Unknown

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<210> 8
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<212> DNA
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<210> 9
<211> 29
<212> DNA
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<210> 10
<211> 14
<212> PRT
<213> Unknown

<220>
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is not available.

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